

*Open**1644**P#7*

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/900,590A

DATE: 01/03/2002
TIME: 11:31:32

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APR 01 2002

Input Set : N:\Crf3\RULE60\09900590A.raw
Output Set: N:\CRF3\01032002\I900590A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Huse, William D.
6 Glaser, Scott M.
8 (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
9 Antibodies, Nucleic Acids Encoding Same and Methods of

Use

11 (iii) NUMBER OF SEQUENCES: 100
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Campbell & Flores LLP
15 (B) STREET: 4370 La Jolla Village Drive, Suite 700
16 (C) CITY: San Diego
17 (D) STATE: California
18 (E) COUNTRY: United States
19 (F) ZIP: 92122
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

C--> 27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/09/900,590A
C--> 29 (B) FILING DATE: 06-Jul-2001

30 (C) CLASSIFICATION:
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 09/016,061
34 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Campbell, Cathryn A.
38 (B) REGISTRATION NUMBER: 31,815
39 (C) REFERENCE/DOCKET NUMBER: P-IX 2965

41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (619) 535-9001
43 (B) TELEFAX: (619) 535-8949

46 (2) INFORMATION FOR SEQ ID NO: 1:
48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 351 base pairs
50 (B) TYPE: nucleic acid
51 (C) STRANDEDNESS: both
52 (D) TOPOLOGY: linear

55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 1..351

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG 48
63 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
64 1 5 10 15
66 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT 96

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67	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	
68				20					25					30			
70	GAC	ATG	TCT	TGG	GTT	CGC	CAG	GCT	CCG	GGC	AAG	GGT	CTG	GAG	TGG	GTC	144
71	Asp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
72				35					40				45				
74	GCA	AAA	GTT	AGT	AGT	GGT	GGT	AGC	ACC	TAC	TAT	TTA	GAC	ACT	GTG		192
75	Ala	Lys	Val	Ser	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Leu	Asp	Thr	Val		
76		50				55			60								
78	CAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAT	AGT	AAG	AAC	ACC	CTA	TAC	240
79	Gln	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	
80	65				70					75			80				
82	CTG	CAA	ATG	AAC	TCT	CTG	AGA	GCC	GAG	GAC	ACA	GCC	GTG	TAT	TAC	TGT	288
83	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
84		85				90			95								
86	GCA	AGA	CAT	AAC	TAC	GGC	AGT	TTT	GCT	TAC	TGG	GGC	CAA	GGG	ACT	ACA	336
87	Ala	Arg	His	Asn	Tyr	Gly	Ser	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	
88				100					105			110					
90	GTG	ACT	GTT	TCT	AGT												351
91	Val	Thr	Val	Ser	Ser												
92		115															

95 (2) INFORMATION FOR SEQ ID NO: 2:

97 (i) SEQUENCE CHARACTERISTICS:
98 (A) LENGTH: 117 amino acids
99 (B) TYPE: amino acid
100 (D) TOPOLOGY: linear

102 (ii) MOLECULE TYPE: protein

104 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

106	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
107	1				5				10			15				
109	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr
110			20						25			30				
112	Asp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
113		35				40			45							
115	Ala	Lys	Val	Ser	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Leu	Asp	Thr	Val	
116		50				55			60							
118	Gln	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
119	65				70				75			80				
121	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
122		85				90			95							
124	Ala	Arg	His	Asn	Tyr	Gly	Ser	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
125		100				105			110							

127 Val Thr Val Ser Ser

128 115

130 (2) INFORMATION FOR SEQ ID NO: 3:

132 (i) SEQUENCE CHARACTERISTICS:
133 (A) LENGTH: 321 base pairs
134 (B) TYPE: nucleic acid
135 (C) STRANDEDNESS: both
136 (D) TOPOLOGY: linear

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139 (ix) FEATURE:
140 (A) NAME/KEY: CDS
141 (B) LOCATION: 1..321
144 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
146 GAG ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT CTC AGC CCA GGA 48
147 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
148 1 5 10 15
150 GAA AGG GCG ACT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC 96
151 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
152 20 25 30
154 CTA CAC TGG TAT CAA CAA AGG CCT GGT CAA GCC CCA AGG CTT CTC ATC 144
155 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
156 35 40 45
158 AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC GCC AGG TTC AGT GGC 192
159 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
160 50 55 60
162 AGT GGA TCA GGG ACA GAT TTC ACC CTC ACT ATC TCC AGT CTG GAG CCT 240
163 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
164 65 70 75 80
166 GAA GAT TTT GCA GTC TAT TAC TGT CAA CAG AGT GGC AGC TGG CCT CAC 288
167 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
168 85 90 95
170 ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG 321
171 Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
172 100 105
175 (2) INFORMATION FOR SEQ ID NO: 4:
177 (i) SEQUENCE CHARACTERISTICS:
178 (A) LENGTH: 107 amino acids
179 (B) TYPE: amino acid
180 (D) TOPOLOGY: linear
182 (ii) MOLECULE TYPE: protein
184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
186 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
187 1 5 10 15
189 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
190 20 25 30
192 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
193 35 40 45
195 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
196 50 55 60
198 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
199 65 70 75 80
201 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
202 85 90 95
204 Thr Phe Gly Gly Thr Lys Val Glu Ile Lys
205 100 105
207 (2) INFORMATION FOR SEQ ID NO: 5:
209 (i) SEQUENCE CHARACTERISTICS:
210 (A) LENGTH: 351 base pairs

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Input Set : N:\Crf3\RULE60\09900590A.raw
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211 (B) TYPE: nucleic acid
212 (C) STRANDEDNESS: both
213 (D) TOPOLOGY: linear
216 (ix) FEATURE:
217 (A) NAME/KEY: CDS
218 (B) LOCATION: 1..351
221 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
223 GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA AGG 48
224 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
225 1 5 10 15
227 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT AGC TAT 96
228 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
229 20 25 30
231 GAC ATG TCT TGG GTT CGC CAG ATT CCG GAG AAG AGG CTG GAG TGG GTC 144
232 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
233 35 40 45
235 GCA AAA GTT AGT AGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG 192
236 Ala Lys Val Ser Ser Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
237 50 55 60
239 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTA TAC 240
240 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
241 65 70 75 80
243 CTG CAA ATG AGC AGT CTG AAC TCT GAG GAC ACA GCC ATG TAT TAC TGT 288
244 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
245 85 90 95
247 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT CTG 336
248 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
249 100 105 110
251 GTC ACT GTC TCT GCA 351
252 Val Thr Val Ser Ala
253 115
256 (2) INFORMATION FOR SEQ ID NO: 6:
258 (i) SEQUENCE CHARACTERISTICS:
259 (A) LENGTH: 117 amino acids
260 (B) TYPE: amino acid
261 (D) TOPOLOGY: linear
263 (ii) MOLECULE TYPE: protein
265 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
267 Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys Pro Gly Arg
268 1 5 10 15
270 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
271 20 25 30
273 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
274 35 40 45
276 Ala Lys Val Ser Ser Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
277 50 55 60
279 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
280 65 70 75 80
282 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys

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283	85	90	95	
285	Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu			
286	100	105	110	
288	Val Thr Val Ser Ala			
289	115			
291	(2) INFORMATION FOR SEQ ID NO: 7:			
293	(i) SEQUENCE CHARACTERISTICS:			
294	(A) LENGTH: 321 base pairs			
295	(B) TYPE: nucleic acid			
296	(C) STRANDEDNESS: both			
297	(D) TOPOLOGY: linear			
300	(ix) FEATURE:			
301	(A) NAME/KEY: CDS			
302	(B) LOCATION: 1..321			
305	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:			
307	GAT ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT GTG ACA CCA GGA	48		
308	Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly			
309	1 5 10 15			
311	GAT AGC GTC AGT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC	96		
312	Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His			
313	20 25 30			
315	CTA CAC TGG TAT CAA CAA AAA TCA CAT GAG TCT CCA AGG CTT CTC ATC	144		
316	Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile			
317	35 40 45			
319	AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC TCC AGG TTC AGT GGC	192		
320	Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly			
321	50 55 60			
323	AGT GGA TCA GGG ACA GAT TTC GCT CTC AGT ATC AAC AGT GTG GAG ACT	240		
324	Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr			
325	65 70 75 80			
327	GAA GAT TTT GGA ATG TAT TTC TGT CAA CAG AGT GGC AGC TGG CCT CAC	288		
328	Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His			
329	85 90 95			
331	ACG TTC GGA GGG GGG ACC AAG CTG GAA ATT AAG	321		
332	Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys			
333	100 105			
336	(2) INFORMATION FOR SEQ ID NO: 8:			
338	(i) SEQUENCE CHARACTERISTICS:			
339	(A) LENGTH: 107 amino acids			
340	(B) TYPE: amino acid			
341	(D) TOPOLOGY: linear			
343	(ii) MOLECULE TYPE: protein			
345	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:			
347	Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly			
348	1 5 10 15			
350	Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His			
351	20 25 30			
353	Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile			
354	35 40 45			

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31

L:773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32